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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,937

DATE: 05/14/2002

TIME: 15:00:19

Input Set : N:\Crf3\RULE60\10038937.txt
 Output Set: N:\CRF3\05142002\J038937.raw

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
 - 5 (i) APPLICANT: Daggett, Lorrie P.
Lu, Chin-Chun
 - 9 (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
 - 12 (iii) NUMBER OF SEQUENCES: 63
 - 14 (iv) CORRESPONDENCE ADDRESS:
 - 15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
 - 16 (B) STREET: 4250 Executive Square, 7th Floor
 - 17 (C) CITY: La Jolla
 - 18 (D) STATE: CA
 - 19 (E) COUNTRY: U.S.A.
 - 20 (F) ZIP: 92037
 - 22 (v) COMPUTER READABLE FORM:
 - 23 (A) MEDIUM TYPE: Floppy disk
 - 24 (B) COMPUTER: IBM PC compatible
 - 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - 28 (vi) CURRENT APPLICATION DATA:
 - 29 (A) APPLICATION NUMBER: US/10/038,937
 - C--> 30 (B) FILING DATE: 18-Apr-2002
 - 45 (C) CLASSIFICATION:
 - 42 (vii) PRIOR APPLICATION DATA:
 - 33 (A) APPLICATION NUMBER: 08/935,105
 - 34 (B) FILING DATE: 29-SEPT-97
 - 38 (A) APPLICATION NUMBER: US 08/231,193
 - 39 (B) FILING DATE: 20-APR-1994
 - 43 (A) APPLICATION NUMBER: US 08/052,449
 - 44 (B) FILING DATE: 20-APR-1993
 - 47 (viii) ATTORNEY/AGENT INFORMATION:
 - 48 (A) NAME: Seidman, Stephanie
 - 49 (B) REGISTRATION NUMBER: 33,779
 - 50 (C) REFERENCE/DOCKET NUMBER: 6362-9383D
 - 52 (ix) TELECOMMUNICATION INFORMATION:
 - 53 (A) TELEPHONE: 619-238-0999
 - 54 (B) TELEFAX: 619-238-0062
- 57 (2) INFORMATION FOR SEQ ID NO: 1:
 - 59 (i) SEQUENCE CHARACTERISTICS:
 - 60 (A) LENGTH: 4298 base pairs
 - 61 (B) TYPE: nucleic acid
 - 62 (C) STRANDEDNESS: both
 - 63 (D) TOPOLOGY: both

ENTERED

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65 (ii) MOLECULE TYPE: cDNA
 68 (ix) FEATURE:
 69 (A) NAME/KEY: CDS
 70 (B) LOCATION: 262..3078
 72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 74 CAAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGGACA GCGCCGGCCG 60
 76 CGTGGGGCTG AGCGCGGAGC CCGCGCGAC GCTTCAGCCC CCCTTCCTC GCGCGACGIC 120
 78 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGAGCC CGCGGGGCCG GCGGAGCGCA 180
 80 GGACGGCCCCG GAAGCCCCGC CGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG 240
 82 CCAGGGCCCCG GCAGCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
 83 Met Ser Thr Met Arg Leu Leu Thr Leu Ala
 84 1 5 10
 86 CTG CTG TIC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
 87 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
 88 15 20 25
 90 GTC AAC ATI GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
 91 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
 92 30 35 40
 94 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
 95 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
 96 45 50 55
 98 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG AAC CCC AAC GCC CAG ATG 483
 99 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
 100 60 65 70
 102 GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
 103 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
 104 75 80 85 90
 106 CTA GTT AGC CAI CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
 107 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
 108 95 100 105
 110 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
 111 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
 112 110 115 120
 114 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675
 115 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu
 116 125 130 135
 118 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG 723
 119 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met
 120 140 145 150
 122 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC 771
 123 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp
 124 155 160 165 170
 126 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG 819
 127 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu
 128 175 180 185
 130 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG 867
 131 Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys
 132 190 195 200
 134 AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC 915

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135	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
136		205			210			215									
138	AIC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
139	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
140		220			225			230									
142	GCC	GCG	ATG	CIG	AAC	AIG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CIG	GIC	GGC	1011
143	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Irp	Leu	Val	Gly	
144	235		240			245			250								
147	GAG	CGC	GAG	AIC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059
148	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	
149		255			260			265									
151	CTC	GGG	CTG	CAG	CTC	AIC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107
152	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	
153		270			275			280									
155	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155
156	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	
157		285			290			295									
159	GAG	AAC	ATC	ACC	GAC	CGG	CCG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC		1203
160	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	
161		300			305			310									
163	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251
164	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	
165	315		320			325			330								
167	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299
168	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	
169		335			340			345									
171	AAG	TTC	GCC	AAC	IAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347
172	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	
173		350			355			360									
175	CAA	GTG	GGC	ATC	IAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	1395
176	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	
177		365			370			375									
179	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443
180	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	
181		380			385			390									
183	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491
184	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	
185	395		400			405			410								
187	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539
188	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	
189		415			420			425									
191	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	1587
192	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	
193		430			435			440									
195	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	1635
196	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	
197		445			450			455									
199	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683
200	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	

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201	460	465	470														
203	GAG	GIG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
204	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
205	475				480				485						490		
207	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CIG	CTC	1779
208	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
209					495				500						505		
211	AGC	GGG	CAG	GCA	GAC	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG		1827
212	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
213					510				515						520		
215	CGC	GCG	CAG	IAC	AIC	GAG	TTT	TCC	AAG	CCC	ITC	AAG	IAC	CAG	GGC	CTG	1875
216	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
217					525				530						535		
219	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923
220	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
221					540				545						550		
223	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
224	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
225					555				560						565		570
227	CAC	GTG	GTG	GCC	GTG	ATG	CTG	CTG	GAC	CGC	TTC	AGC	CCC	ITC		2019	
228	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
229					575				580						585		
231	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC		2067
232	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	
233					590				595						600		
235	CTG	TCC	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC		2115
236	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
237					605				610						615		
239	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
240	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
241					620				625						630		
243	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
244	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
245					635				640						645		650
247	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259
248	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
249					655				660						665		
251	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
252	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
253					670				675						680		
255	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
256	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
257					685				690						695		
259	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
260	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
261					700				705						710		
263	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
264	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	
265	715				720				725						730		

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267	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
268	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	
269					735				740						745		
271	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	ATG	2547
272	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	
273					750				755						760		
275	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCG	TCG	ATC	CTC	AAG		2595
276	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	
277					765				770						775		
279	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CIG	GAC	AAG	ACG	TGG	GTT	CGG	2643
280	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Ihr	Irp	Val	Arg	
281					780				785						790		
283	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ATC	TTT	2691
284	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Ihr	Phe	
285	795				800				805						810		
287	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	2739
288	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	
289					815				820						825		
291	GGG	AIC	ITC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	2787
292	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Fyr	Lys	Arg	His	Lys	Asp	
293					830				835						840		
295	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	2835
296	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	
297					845				850						855		
299	CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	2883
300	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	
301					860				865						870		
303	AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	2931
304	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Ihr	Ser	Ihr	Leu	Ala	Ser	Ser	
305	875				880				885						890		
307	TTC	AAG	AGG	CGT	AGG	TCC	TCC	AAA	GAC	ACG	AGC	ACC	GGG	GGT	GGA	CGC	2979
308	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Arg		
309					895				900						905		
311	GTC	GCT	TTG	CAA	AAC	CAA	AAA	GAC	ACA	GIG	CTG	CCG	CGA	CGC	GCT	ATT	3027
312	Gly	Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	
313					910				915						920		
315	GAG	AGG	GAG	GAG	GGC	CAG	CTG	CAG	CTG	TGT	TCC	CGT	CAT	AGG	GAG	AGC	3075
316	Glu	Arg	Glu	Gly	Gly	Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser	
317					925				930						935		
319	TGAGACTCCC	CGCCCCGCCCT	CCTCTGCCCC	CCTCCCCCGCA	SACAGACAGA	CAGACGGACG											3135
321	GGACAGCGGC	CCGGCCCCACCG	CAGAGCCCCCG	GAGCACCCACG	GGGTGCGGGGG	AGGAGCACC											3195
323	CCAGCCTCCC	CCAGGCTGCG	CCTGCCCGGCC	CGCCGGTTGG	CGGGCTGGCC	GGTCCACCCC											3255
325	GTCCCCGGCCCC	CGCGCGTGCC	CCCAGCGTGG	GGCTAACGGG	CGCCTTGCT	GTGTATTCT											3315
327	ATTTTGCGACG	AGTACCATCC	CACTGATAIC	ACGGGCCCCGC	TCAACCTCTC	AGATCCCCTG											3375
329	GTCAGCACCG	TGGTGTGAGG	CCCCCGGAGG	CGCCCCACCTG	CGCAGTTAGC	CCGGCCAAGG											3435
331	ACACTGATGG	GTCCTGCTGC	TCGGGAAGGC	CTGAGGGAAG	CCCACCCGCC	CCAGAGACTG											3495
333	CCCACCCCTGG	GCCTCCCGTC	CGTCCGCCCG	CCCACCCCGC	TGCCCTGGCG	GCAGCCCCCTG											3555
335	CTGGACCAAG	GTGCGGACCG	GAGCGGGCTGA	GGACGGGGCA	GAGCTGAGTC	GGCTGGGGCAG											3615
337	GGCCGCAGGG	CGCTCCGGCA	GAGGCAGGCC	CCTGGGGTCT	CTGAGCAGTG	GGGAGCGGGGG											3675

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18
Seq#:47; N Pos. 18
Seq#:49; N Pos. 18
Seq#:51; N Pos. 18
Seq#:53; N Pos. 18
Seq#:57; Xaa Pos.1147,1171
Seq#:58; Xaa Pos.1147,1171

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10038937.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1631 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:2123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:2199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:4013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:4109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/038,937

DATE: 05/14/2002

TIME: 15:00:20

Input Set : N:\Crf3\RULE60\10038937.txt
Output Set: N:\CRF3\05142002\J038937.raw

L:4375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:4379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:4383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:4387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:12994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:3937
L:13002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:4033
L:13277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1136
L:13283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1168